GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:26:12 ; Search time 27 Seconds
(without alignments)
837.207 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 545
Sequence: 1 MAKEIKFSADARAAMVRGVD.....TPAPAMPAGMDPGMMGGMGG 545

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 8

Total number of hits satisfying chosen parameters: 222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	538	98.7	542	1	CH60_STRPY	P82485 streptococc
2	56	10.3	542	1	CH60_LACLA	P37282 lactococcus
3	32	5.9	540	1	CH60_LACHE	O68324 lactobacill
4	31	5.7	542	1	CH60_LISMO	Q9age6 listeria mo
5	27	5.0	544	1	CH60_AGRT5	P30779 agrobacteri
6	27	5.0	545	1	CH61_RHIME	P35469 rhizobium m
7	27	5.0	545	1	CH64_RHIME	Q92zq4 rhizobium m
8	27	5.0	547	1	CH60_BORPE	P48210 bordetella
9	26	4.8	538	1	CH60_STAAU	Q08854 staphylococ
10	26	4.8	542	1	CH60_LISIN	Q929v0 listeria in
11	26	4.8	542	1	CH65_RHIME	P35471 rhizobium m
12	25	4.6	539	1	CH60_BACST	Q07201 bacillus st
13	25	4.6	540	1	CH60_CLOTM	P48212 clostridium
14	25	4.6	544	1	CH60_BACHD	O50305 bacillus ha
15	25	4.6	546	1	CH60_BURCE	Q9zfe0 burkholderi
16	25	4.6	546	1	CH60_BURPS	Q9f712 burkholderi
17	25	4.6	546	1	CH60_BURTH	P58723 burkholderi
18	25	4.6	546	1	CH60_BURVI	Q9zfd8 burkholderi
19	24	4.4	538	1	CH60_BACP3	P26209 bacillus ps
20	24	4.4	539	1	CH61_BRAJA	P77829 bradyrhizob
21	24	4.4	543	1	CH60_BACSU	P28598 bacillus su
22	24	4.4	543	1	CH60_CHLMU	Q59322 chlamydia m
23	24	4.4	543	1	CH60_CHLTR	P17203 chlamydia t
24	24	4.4	544	1	CH60_CHLPN	P31681 chlamydia p
25	24	4.4	544	1	CH60_CHLPS	P15599 chlamydia p
26	24	4.4	545	1	CH60_CAMJE	O69289 campylobact
27	24	4.4	545	1	CH60_PORGI	P42375 porphyromon
28	24	4.4	546	1	CH60_BRUAB	P25967 brucella ab
29	23	4.2	543	1	CH60_CLOAB	P30717 clostridium
30	23	4.2	545	1	CH60_PSEPU	P48216 pseudomonas
31	23	4.2	546	1	CH60_CHRVI	P31293 chromatium
32	23	4.2	547	1	CH60_CAUCR	P48211 caulobacter
33	23	4.2	547	1	CH60_PSEAE	P30718 pseudomonas
34	22	4.0	529	1	CH60_GUITH	O78419 guillardia
35	22	4.0	547	1	CH60_BARHE	O33963 bartonella
36	22	4.0	547	1	CH60_BARQU	O33964 bartonella
37	22	4.0	548	1	CH60_ZYMMO	P48220 zymomonas m
38	22	4.0	585	1	CH60_PYRSA	P46224 pyrenomonas
39	21	3.9	540	1	CH61_SYNY3	Q05972 synechocyst
40	21	3.9	541	1	CH60_CYAPA	Q37757 cyanophora
41	21	3.9	544	1	CH61_SYNVU	O50383 synechococc
42	21	3.9	552	1	CH60_COXBU	P19421 coxiella bu
43	21	3.9	552	1	CH60_PSEST	O33500 pseudomonas
44	20	3.7	539	1	CH62_MYCTU	P06806 mycobacteri
45	20	3.7	540	1	CH60_MYCPA	P42384 mycobacteri
46	20	3.7	540	1	CH62_MYCLE	P09239 mycobacteri
47	20	3.7	543	1	CH60_BARBA	P35635 bartonella
48	20	3.7	546	1	CH60_RHILV	P34939 rhizobium l
49	19	3.5	300	1	CH60_SYNP6	P12834 synechococc
50	19	3.5	540	1	CH60_THEBR	Q60024 thermoanaer
51	19	3.5	542	1	CH62_RHIME	P35470 rhizobium m
52	19	3.5	544	1	CH60_SYNP7	P22879 synechococc
53	19	3.5	545	1	CH63_BRAJA	P35862 bradyrhizob
54	19	3.5	546	1	CH60_LEPIN	P35468 leptospira
55	19	3.5	549	1	CH62_BRAJA	P35861 bradyrhizob
56	18	3.3	538	1	CH60_STAEP	P48218 staphylococ
57	18	3.3	542	1	CH60_THETH	P45746 thermus the
58	18	3.3	544	1	CH60_FRATU	P94798 francisella
59	17	3.1	539	1	CH61_MYCTU	Q59573 mycobacteri
60	17	3.1	544	1	CH63_RHIME	Q930y0 rhizobium m
61	16	2.9	476	1	CH62_STRLI	O33658 streptomyce
62	16	2.9	539	1	CH60_CLOPE	P26821 clostridium
63	16	2.9	539	1	CH61_STRAL	Q00767 streptomyce
64	16	2.9	539	1	CH62_STRAL	Q00768 streptomyce
65	16	2.9	540	1	CH61_STRCO	P40171 streptomyce
66	16	2.9	540	1	CH61_STRLI	O33659 streptomyce
67	16	2.9	543	1	CH60_MYCGE	P47632 mycoplasma
68	16	2.9	543	1	CH60_MYCPN	P78012 mycoplasma
69	16	2.9	544	1	CH60_NEIFL	P48215 neisseria f
70	16	2.9	544	1	CH60_NEIGO	P29842 neisseria g
71	16	2.9	544	1	CH60_NEIMA	P57006 neisseria m
72	16	2.9	544	1	CH60_NEIMB	P42385 neisseria m
73	16	2.9	548	1	CH60_EHRRI	P48214 ehrlichia r
74	16	2.9	548	1	CH60_EHRSE	O32606 ehrlichia s
75	15	2.8	534	1	CH60_GALSU	P28256 galdieria s
76	15	2.8	539	1	CH60_ENTAG	O66200 enterobacte
77	15	2.8	539	1	CH60_ENTAM	O66196 enterobacte
78	15	2.8	539	1	CH60_ENTAS	O66190 enterobacte
79	15	2.8	539	1	CH60_ENTIT	O66192 enterobacte
80	15	2.8	539	1	CH60_SERRU	O66202 serratia ru
81	15	2.8	540	1	CH60_ENTAE	O66198 enterobacte
82	15	2.8	540	1	CH60_ENTGE	O66194 enterobacte
83	15	2.8	540	1	CH60_ERWAP	O66222 erwinia aph
84	15	2.8	540	1	CH60_ERWCA	O66220 erwinia car
85	15	2.8	540	1	CH60_KLEON	O66214 klebsiella
86	15	2.8	540	1	CH60_KLEOX	O66210 klebsiella
87	15	2.8	540	1	CH60_KLEPL	O66212 klebsiella
88	15	2.8	540	1	CH60_SERFI	O66204 serratia fi
89	15	2.8	541	1	CH60_ERWHE	O66216 erwinia her
90	15	2.8	541	1	CH60_PANAN	O66218 pantoea ana
91	15	2.8	544	1	CH60_AERSA	O68309 aeromonas s
92	15	2.8	545	1	CH60_BORBU	P27575 borrelia bu
93	15	2.8	545	1	CH60_PARDE	Q9z462 paracoccus
94	15	2.8	545	1	CH60_RHOCA	P95678 rhodobacter
95	15	2.8	545	1	CH60_SODGL	Q9anr8 sodalis glo
96	15	2.8	546	1	CH60_ACTAC	P46398 actinobacil
97	15	2.8	546	1	CH60_ACTPL	P94166 actinobacil
98	15	2.8	546	1	CH60_LEGMI	P26194 legionella
99	15	2.8	546	1	CH60_WIGGL	Q9anr9 wiggleswort
100	15	2.8	546	1	CH61_RHOSH	P20110 rhodobacter
101	15	2.8	547	1	CH60_ALTHA	Q9xau7 alteromonas
102	15	2.8	547	1	CH60_ECOLI	P06139 escherichia
103	15	2.8	547	1	CH60_HAEDU	P31294 haemophilus
104	15	2.8	547	1	CH60_KLEPN	O66026 klebsiella
105	15	2.8	547	1	CH60_LEGPN	P26878 legionella
106	15	2.8	547	1	CH60_PASMU	Q59687 pasteurella

107	15	2.8	547	1	CH60_SALTY	P48217 salmonella
108	15	2.8	548	1	CH60_BUCAI	P25750 buchnera ap
109	15	2.8	548	1	CH60_BUCMP	O51832 buchnera ap
110	15	2.8	548	1	CH60_HAEIN	P43733 haemophilus
111	15	2.8	548	1	CH60_XANMA	P95800 xanthomonas
112	15	2.8	550	1	CH60_YEREN	P48219 yersinia en
113	15	2.8	551	1	CH60_AMOPS	P26004 amoeba prot
114	15	2.8	551	1	CH60_BUCAP	Q59177 buchnera ap
115	15	2.8	566	1	HS60_CANAL	O74261 candida alb
116	15	2.8	569	1	CH63_HELVI	P25420 heliothis v
117	15	2.8	573	1	CH60_CRIGR	P18687 cricetulus
118	15	2.8	573	1	CH60_DROME	O02649 drosophila
119	15	2.8	573	1	CH60_HUMAN	P10809 homo sapien
120	15	2.8	573	1	CH60_MOUSE	P19226 mus musculu
121	15	2.8	573	1	CH6C_DROME	Q9vmn5 drosophila
122	14	2.6	40	1	CH60_BACFO	P81284 bacteroides
123	14	2.6	408	1	CH60_RICRI	O34198 rickettsia
124	14	2.6	426	1	CH60_RICTY	O85754 rickettsia
125	14	2.6	435	1	RUBB_CHLRE	Q42693 chlamydomon
126	14	2.6	528	1	CH60_ODOSI	P49464 odontella s
127	14	2.6	528	1	CH60_PORPU	P51349 porphyra pu
128	14	2.6	537	1	CH61_MYCLE	P37578 mycobacteri
129	14	2.6	538	1	CH60_THEMA	Q9wyx6 thermotoga
130	14	2.6	540	1	CH60_SERMA	O66206 serratia ma
131	14	2.6	540	1	CH60_TROWH	Q9kjc0 tropheryma
132	14	2.6	541	1	CH62_RHOSH	P95647 rhodobacter
133	14	2.6	543	1	CH62_SYNVU	Q57002 synechococc
134	14	2.6	546	1	RUB1_BRANA	P21239 brassica na
135	14	2.6	548	1	CH60_RICCN	Q92h04 rickettsia
136	14	2.6	550	1	CH60_RICPR	Q9zct7 rickettsia
137	14	2.6	551	1	CH62_SYNY3	P22034 synechocyst
138	14	2.6	572	1	HS60_YEAST	P19882 saccharomyc
139	14	2.6	590	1	HS60_AJECA	P50142 ajellomyces
140	14	2.6	592	1	HS60_PARBR	O60008 paracoccidi
141	13	2.4	543	1	CH60_TREPA	P23033 treponema p
142	13	2.4	546	1	CH60_HELPJ	Q9zn50 helicobacte
143	13	2.4	546	1	CH60_HELPY	P42383 helicobacte
144	13	2.4	588	1	RUBB_BRANA	P21241 brassica na
145	13	2.4	595	1	RUBB_PEA	P08927 pisum sativ
146	13	2.4	600	1	RUBB_ARATH	P21240 arabidopsis
147	12	2.2	259	1	RUBC_CHLRE	Q42695 chlamydomon
148	12	2.2	410	1	CH60_EHRCA	O34194 ehrlichia c
149	12	2.2	470	1	CH60_TRIVA	Q95058 trichomonas
150	12	2.2	541	1	CH60_ANAPH	O34191 anaplasma p
151	12	2.2	545	1	CH60_AQUAE	O67943 aquifex aeo
152	12	2.2	550	1	CH60_EHRCH	P42382 ehrlichia c
153	12	2.2	551	1	CH60_COWRU	P48213 cowdria rum
154	12	2.2	555	1	CH60_RICTS	P16625 rickettsia
155	12	2.2	582	1	HS60_SCHPO	Q09864 schizosacch
156	11	2.0	114	1	CH60_MYCUL	Q50826 mycobacteri
157	11	2.0	120	1	CH60_MYCAG	Q48883 mycobacteri
158	11	2.0	120	1	CH60_MYCAS	Q48884 mycobacteri
159	11	2.0	120	1	CH60_MYCCI	Q49025 mycobacteri
160	11	2.0	120	1	CH60_MYCFA	Q49155 mycobacteri
161	11	2.0	120	1	CH60_MYCGN	Q49374 mycobacteri
162	11	2.0	120	1	CH60_MYCGO	Q49375 mycobacteri
163	11	2.0	120	1	CH60_MYCGS	Q49373 mycobacteri
164	11	2.0	120	1	CH60_MYCIT	Q49564 mycobacteri
165	11	2.0	120	1	CH60_MYCKA	Q49594 mycobacteri
166	11	2.0	120	1	CH60_MYCMA	Q50212 mycobacteri
167	11	2.0	120	1	CH60_MYCNO	Q50255 mycobacteri
168	11	2.0	120	1	CH60_MYCPH	Q50270 mycobacteri
169	11	2.0	120	1	CH60_MYCPV	Q50271 mycobacteri
170	11	2.0	120	1	CH60_MYCRH	Q50373 mycobacteri
171	11	2.0	120	1	CH60_MYCSC	Q50382 mycobacteri
172	11	2.0	120	1	CH60_MYCSH	Q50383 mycobacteri
173	11	2.0	120	1	CH60_MYCVA	Q50827 mycobacteri
174	11	2.0	120	1	CH60_MYCXE	Q50852 mycobacteri
175	11	2.0	151	1	CH60_MYCAV	Q48900 mycobacteri
176	11	2.0	151	1	CH60_MYCCH	Q49093 mycobacteri
177	11	2.0	151	1	CH60_MYCFO	Q49160 mycobacteri
178	11	2.0	151	1	CH60_MYCMR	Q50220 mycobacteri
179	11	2.0	499	1	RUBB_SECCE	Q43831 secale cere
180	11	2.0	530	1	CH60_CYACA	Q9tlz1 cyanidium c
181	11	2.0	554	1	CH60_HOLOB	P94820 holospora o
182	11	2.0	562	1	CH60_TRYBB	Q37683 trypanosoma
183	11	2.0	562	1	CH60_TRYCR	Q95046 trypanosoma
184	11	2.0	568	1	CH60_CAEEL	P50140 caenorhabdi
185	11	2.0	569	1	CH60_EUGGR	Q39727 euglena gra
186	11	2.0	583	1	RUB2_BRANA	P34794 brassica na
187	11	2.0	586	1	RUBA_ARATH	P21238 arabidopsis
188	11	2.0	589	1	CH60_LEIMA	Q94596 leishmania
189	11	2.0	648	1	CH6B_DROME	Q9vps5 drosophila
190	10	1.8	495	1	RUBA_RICCO	P08824 ricinus com
191	10	1.8	543	1	RUBA_WHEAT	P08823 triticum ae
192	10	1.8	575	1	CH61_CUCMA	Q05045 cucurbita m
193	10	1.8	575	1	CH62_CUCMA	Q05046 cucurbita m
194	10	1.8	576	1	CH62_MAIZE	Q43298 zea mays (m
195	10	1.8	577	1	CH60_ARATH	P29197 arabidopsis
196	10	1.8	577	1	CH61_MAIZE	P29185 zea mays (m
197	10	1.8	580	1	RUBA_CHLRE	Q42694 chlamydomon
198	10	1.8	587	1	CH60_BRANA	P35480 brassica na
199	10	1.8	587	1	RUBA_PEA	P08926 pisum sativ
200	9	1.7	47	1	CH60_LEITA	P56281 leishmania
201	8	1.5	40	1	CH60_SOLTU	P80502 solanum tub
202	8	1.5	355	1	YDP6_SCHPO	O14009 schizosacch
203	8	1.5	441	1	ZRAR_SALTI	Q8z333 salmonella
204	8	1.5	441	1	ZRAR_SALTY	P25852 salmonella
205	8	1.5	542	1	THSA_METTH	O26320 methanobact
206	8	1.5	543	1	THSB_THEAC	P48425 thermoplasm
207	8	1.5	545	1	THSA_ARCFU	O28045 archaeoglob
208	8	1.5	545	1	THSB_ARCFU	O28821 archaeoglob
209	8	1.5	545	1	THSB_THEK8	O24732 thermococcu
210	8	1.5	545	1	THS_DESSY	Q53546 desulfuroco
211	8	1.5	546	1	THSB_PYRKO	O52500 pyrococcus
212	8	1.5	546	1	THSB_THEK1	O24730 thermococcu
213	8	1.5	548	1	THSA_PYRKO	O24729 pyrococcus
214	8	1.5	549	1	THSA_THEK8	O24731 thermococcu
215	8	1.5	549	1	THS_PYRHO	O57762 pyrococcus
216	8	1.5	550	1	THS_PYRAB	Q9v2q7 pyrococcus
217	8	1.5	556	1	THSB_HALN1	Q9hni0 halobacteri
218	8	1.5	557	1	THS2_HALVO	O30560 halobacteri
219	8	1.5	700	1	CH60_PLAFG	P34940 plasmodium
220	8	1.5	946	1	AMPN_PLUXY	P91887 plutella xy
221	8	1.5	1286	1	RPOD_GUITH	O78483 guillardia
222	8	1.5	1520	1	ABL_DROME	P00522 drosophila

ALIGNMENTS

```
RESULT 1
CH60_STRPY
ID   CH60_STRPY     STANDARD;      PRT;   542 AA.
AC   P82485;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL OR SPY2070.
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX   MEDLINE=21192684; PubMed=11296296;
RA   Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA   Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA   Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
RA   Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT   "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN   [2]
RP   PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
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RC   STRAIN=JRS4 / Serotype M6;
RA   Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA   VanBogelen R.A.;
RT   "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT   proteins.";
RL   Submitted (MAY-2000) to the SWISS-PROT data bank.
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   ---------------------------------------------------------------------
DR   EMBL; AE006627; AAK34727.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; Heat shock; ATP-binding; Complete proteome.
FT   INIT_MET      0      0
SQ   SEQUENCE   542 AA;  56964 MW;  C7B9A139B6FD71D4 CRC64;

  Query Match             98.7%;  Score 538;  DB 1;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  538;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 IKFSADARAAMVRGVDMLADTVKVTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDH 64
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Db       4 IKFSADARAAMVRGVDMLADTVKVTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDH 63

Qy      65 FENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEGLKNVTAGANPIGIRRGIETATA 124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEGLKNVTAGANPIGIRRGIETATA 123

Qy     125 TAVEALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETE 184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 TAVEALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETE 183

Qy     185 LEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRP 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRP 243

Qy     245 LLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITEDLG 304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 LLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITEDLG 303

Qy     305 LELKDATMTALGQAAKITVDKDSTVIVEGSGSSEAIANRIALIKSQLETTTSDFDREKLQ 364
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 LELKDATMTALGQAAKITVDKDSTVIVEGSGSSEAIANRIALIKSQLETTTSDFDREKLQ 363

Qy     365 ERLAKLAGGVAVIKVGAPTETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITVIEKV 424
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 ERLAKLAGGVAVIKVGAPTETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITVIEKV 423

Qy     425 AALELEGDDATGRNIVLRALEEPVRQIALNAGYEGSVVIDKLKNSPAGTGFNAATGEWVD 484
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     424 AALELEGDDATGRNIVLRALEEPVRQIALNAGYEGSVVIDKLKNSPAGTGFNAATGEWVD 483

Qy     485 MIKTGIIDPVKVTRSALQNAASVASLILTTEAVVANKPEPATPAPAMPAGMDPGMMGG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 MIKTGIIDPVKVTRSALQNAASVASLILTTEAVVANKPEPATPAPAMPAGMDPGMMGG 541
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RESULT 2
CH60_LACLA
ID   CH60_LACLA     STANDARD;      PRT;   542 AA.
AC   P37282;
DT   01-OCT-1994 (Rel. 30, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL OR LL0394.
OS   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1360;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93252268; PubMed=8486277;
RA   Kim S.G., Batt C.A.;
RT   "Cloning and sequencing of the Lactococcus lactis subsp. lactis
RT   groESL operon.";
RL   Gene 127:121-126(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IL1403;
RX   MEDLINE=21235186; PubMed=11337471;
RA   Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
RA   Weissenbach J., Ehrlich S.D., Sorokin A.;
RT   "The complete genome sequence of the lactic acid bacterium Lactococcus
RT   lactis ssp. lactis IL1403.";
RL   Genome Res. 11:731-753(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X71132; CAA50446.1; -.
DR   EMBL; AE006276; AAK04492.1; -.
DR   PIR; S32106; S32106.
DR   PIR; JN0661; JN0661.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Complete proteome.
FT   CONFLICT     63     63       D -> V (IN REF. 1).
FT   CONFLICT     89     89       T -> N (IN REF. 1).
FT   CONFLICT    289    289       D -> H (IN REF. 1).
FT   CONFLICT    367    367       L -> V (IN REF. 1).
FT   CONFLICT    542    542       M -> I (IN REF. 1).
SQ   SEQUENCE   542 AA;  57201 MW;  D7D6F5319DA59721 CRC64;

  Query Match             10.3%;  Score 56;  DB 1;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-41;
  Matches   56;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      44 GSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIV 99
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      44 GSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIV 99


RESULT 3
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CH60_LACHE
ID   CH60_LACHE     STANDARD;      PRT;   540 AA.
AC   O68324;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL.
OS   Lactobacillus helveticus.
OC   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC   Lactobacillus.
OX   NCBI_TaxID=1587;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LH212;
RX   MEDLINE=98439363; PubMed=9766226;
RA   Broadbent J.R., Oberg C.J., Wei L.;
RT   "Characterization of the Lactobacillus helveticus groESL operon.";
RL   Res. Microbiol. 149:247-253(1998).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF031929; AAC29004.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding.
SQ   SEQUENCE   540 AA;  57638 MW;  4257DDB45FC7C4B4 CRC64;

  Query Match             5.9%;  Score 32;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-20;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    254 GEALPTLVLNKIRGTFNVVAVKAPGFGDRRKA 285
          ||||||||||||||||||||||||||||||||
Db    254 GEALPTLVLNKIRGTFNVVAVKAPGFGDRRKA 285


RESULT 4
CH60_LISMO
ID   CH60_LISMO     STANDARD;      PRT;   542 AA.
AC   Q9AGE6;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR GROEL OR LMO2068.
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LO28 / Serovar 1/2c;
RX   MEDLINE=21246697; PubMed=11349060;
RA   Gahan C.G., O'Mahony J., Hill C.;
RT   "Characterization of the groESL operon in Listeria monocytogenes:
RT   utilization of two reporter systems (gfp and hly) for evaluating in
RT   vivo expression.";
RL   Infect. Immun. 69:3924-3932(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EGD-e / Serovar 1/2a;
RX   MEDLINE=21537279; PubMed=11679669;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF335323; AAK28538.1; -.
DR   EMBL; AL591982; CAD00146.1; -.
DR   HSSP; P06139; 1GRL.
DR   ListiList; LMO02068; -.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Complete proteome.
SQ   SEQUENCE   542 AA;  57367 MW;  9818B45967D92944 CRC64;

  Query Match             5.7%;  Score 31;  DB 1;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-19;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296
          |||||||||||||||||||||||||||||||
Db    266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296


RESULT 5
CH60_AGRT5
ID   CH60_AGRT5     STANDARD;      PRT;   544 AA.
AC   P30779;
DT   01-JUL-1993 (Rel. 26, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL OR ATU0682 OR AGR_C_1220.
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93259955; PubMed=8098329;
RA   Segal G., Ron E.Z.;
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RT   "Heat shock transcription of the groESL operon of Agrobacterium
RT   tumefaciens may involve a hairpin-loop structure.";
RL   J. Bacteriol. 175:3083-3088(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608550; PubMed=11743193;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608551; PubMed=11743194;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; X68263; CAA48331.1; -.
DR   EMBL; AE009036; AAL41698.1; -.
DR   EMBL; AE008002; AAK86491.1; -.
DR   PIR; S23918; S23918.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Complete proteome.
FT   CONFLICT      8      8       F -> P (IN REF. 1).
FT   CONFLICT     10     10       R -> A (IN REF. 1).
FT   CONFLICT     48     48       R -> P (IN REF. 1).
FT   CONFLICT    258    258       A -> R (IN REF. 1).
FT   CONFLICT    513    513       L -> V (IN REF. 1).
SQ   SEQUENCE   544 AA;  57670 MW;  B408D16FD9650046 CRC64;

  Query Match             5.0%;  Score 27;  DB 1;  Length 544;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-16;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
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Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301
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RESULT 6
CH61_RHIME
ID   CH61_RHIME     STANDARD;      PRT;   545 AA.
AC   P35469;
DT   01-JUN-1994 (Rel. 29, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin 1 (Protein Cpn60 1) (groEL protein 1).
GN   GROL1 OR GROEL1 OR GROEL-A OR R00792 OR SMC00913.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=93231539; PubMed=8097179;
RA   Rusanganwa E., Gupta R.S.;
RT   "Cloning and characterization of multiple groEL chaperonin-encoding
RT   genes in Rhizobium meliloti.";
RL   Gene 126:67-75(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RA   Ogawa J.;
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396507; PubMed=11481430;
RA   Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA   Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA   Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA   Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA   Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT   "Analysis of the chromosome sequence of the legume symbiont
RT   Sinorhizobium meliloti strain 1021.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- INDUCTION: BY HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M94192; AAA26285.1; -.
DR   EMBL; U19726; AAA61955.1; -.
DR   EMBL; AL591785; CAC45364.1; -.
DR   PIR; JN0509; JN0509.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock; Multigene family;
KW   Complete proteome.
FT   CONFLICT     12     12       A -> G (IN REF. 1).
SQ   SEQUENCE   545 AA;  57687 MW;  4CEF358957E1B45A CRC64;

  Query Match             5.0%;  Score 27;  DB 1;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-16;
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  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
           |||||||||||||||||||||||||||||
Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301


RESULT 7
CH64_RHIME
ID   CH64_RHIME     STANDARD;      PRT;   545 AA.
AC   Q92ZQ4;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin 4 (Protein Cpn60 4) (groEL protein 4).
GN   GROL4 OR GROEL4 OR RA0395 OR SMA0744.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymA (megaplasmid 1).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396509; PubMed=11481432;
RA   Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA   Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA   Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA   Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA   Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT   "Nucleotide sequence and predicted functions of the entire
RT   Sinorhizobium meliloti pSymA megaplasmid.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; AE007230; AAK65053.1; -.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock; Multigene family; Plasmid;
KW   Complete proteome.
SQ   SEQUENCE   545 AA;  57701 MW;  49BA61F23CE70431 CRC64;

  Query Match             5.0%;  Score 27;  DB 1;  Length 545;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-16;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
           |||||||||||||||||||||||||||||
Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301


RESULT 8
CH60_BORPE
ID   CH60_BORPE     STANDARD;      PRT;   547 AA.
AC   P48210;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL OR CPN60.
OS   Bordetella pertussis.
OC   Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC   Bordetella.
OX   NCBI_TaxID=520;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Tohama / BP338;
RX   MEDLINE=95309719; PubMed=7789805;
RA   Fernandez R.C., Weiss A.A.;
RT   "Cloning and sequencing of the Bordetella pertussis cpn10/cpn60
RT   (groESL) homolog.";
RL   Gene 158:151-152(1995).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12277; AAA74967.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding.
SQ   SEQUENCE   547 AA;  57481 MW;  F780D0401F63CF3F CRC64;

  Query Match             5.0%;  Score 27;  DB 1;  Length 547;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-16;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
           |||||||||||||||||||||||||||||
Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301


RESULT 9
CH60_STAAU
ID   CH60_STAAU     STANDARD;      PRT;   538 AA.
AC   Q08854;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein) (Heat shock protein
DE   60).
GN   GROL OR MOPA OR GROEL OR HSP60.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC   STRAIN=912;
RX   MEDLINE=93290669; PubMed=7916607;
RA   Ohta T., Honda K., Kuroda M., Saito K., Hayashi H.;
RT   "Molecular characterization of the gene operon of heat shock proteins
RT   HSP60 and HSP10 in methicillin-resistant Staphylococcus aureus.";
RL   Biochem. Biophys. Res. Commun. 193:730-737(1993).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
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CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- INDUCTION: BY HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14711; BAA03533.1; -.
DR   PIR; JN0601; JN0601.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock.
FT   INIT_MET      0      0
SQ   SEQUENCE   538 AA;  57722 MW;  58173E21A6EA1C5E CRC64;

  Query Match             4.8%;  Score 26;  DB 1;  Length 538;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     356 SDFDREKLQERLAKLAGGVAVIKVGA 381
           |||||||||||||||||||||||||||
Db     356 SDFDREKLQERLAKLAGGVAVIKVGA 381


RESULT 10
CH60_LISIN
ID   CH60_LISIN     STANDARD;      PRT;   542 AA.
AC   Q929V0;
DT   15-JUN-2002 (Rel. 41, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR GROEL OR LIN2174.
OS   Listeria innocua.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1642;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CLIP 11262 / Serovar 6a;
RX   MEDLINE=21537279; PubMed=11679669;
RA   Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA   Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA   Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA   Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA   Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA   Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA   Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA   Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT   "Comparative genomics of Listeria species.";
RL   Science 294:849-852(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AL596171; CAC97403.1; -.
DR   ListiList; LIN02174; -.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Complete proteome.
SQ   SEQUENCE   542 AA;  57301 MW;  68D6AD2A730DB709 CRC64;

  Query Match             4.8%;  Score 26;  DB 1;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     266 RGTFNVVAVKAPGFGDRRKAMLEDIA 291
           ||||||||||||||||||||||||||
Db     266 RGTFNVVAVKAPGFGDRRKAMLEDIA 291


RESULT 11
CH65_RHIME
ID   CH65_RHIME     STANDARD;      PRT;   542 AA.
AC   P35471;
DT   01-JUN-1994 (Rel. 29, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin 5 (Protein Cpn60 5) (groEL protein 5).
GN   GROL5 OR GROEL5 OR GROEL-C OR RB1006 OR SMB21566.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymB (megaplasmid 2).
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=93231539; PubMed=8097179;
RA   Rusanganwa E., Gupta R.S.;
RT   "Cloning and characterization of multiple groEL chaperonin-encoding
RT   genes in Rhizobium meliloti.";
RL   Gene 126:67-75(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396508; PubMed=11481431;
RA   Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA   Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA   Golding B., Puehler A.;
RT   "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT   fixing endosymbiont Sinorhizobium meliloti.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- INDUCTION: BY HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; M94191; AAA26287.1; -.
DR   EMBL; AL603645; CAC49406.1; -.
DR   PIR; JN0512; JN0512.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock; Multigene family; Plasmid;
KW   Complete proteome.
FT   CONFLICT    239    239       A -> R (IN REF. 1).
FT   CONFLICT    400    400       L -> V (IN REF. 1).
FT   CONFLICT    504    504       A -> G (IN REF. 1).
FT   CONFLICT    534    538       LPAGG -> FRPR (IN REF. 1).
SQ   SEQUENCE   542 AA;  57882 MW;  200FAC54B6736245 CRC64;

  Query Match             4.8%;  Score 26;  DB 1;  Length 542;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    273 AVKAPGFGDRRKAMLEDIAILTGGTV 298
          |||||||||||||||||||||||||
Db    275 AVKAPGFGDRRKAMLEDIAILTGGTV 300


RESULT 12
CH60_BACST
ID   CH60_BACST     STANDARD;      PRT;   539 AA.
AC   Q07201;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL.
OS   Bacillus stearothermophilus.
OC   Bacteria; Firmicutes; Bacillales; Geobacillus.
OX   NCBI_TaxID=1422;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NUB36;
RX   MEDLINE=93224474; PubMed=8096841;
RA   Schoen U., Schumann W.;
RT   "Molecular cloning, sequencing, and transcriptional analysis of the
RT   groESL operon from Bacillus stearothermophilus.";
RL   J. Bacteriol. 175:2465-2469(1993).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- INDUCTION: BY HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; L10132; AAA22752.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock.
SQ   SEQUENCE   539 AA;  57244 MW;  37FE4A0D7492CC3E CRC64;

  Query Match             4.6%;  Score 25;  DB 1;  Length 539;
  Best Local Similarity   100.0%;  Pred. No. 3e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    272 VAVKAPGFGDRRKAMLEDIAILTGG 296
          |||||||||||||||||||||||||
Db    272 VAVKAPGFGDRRKAMLEDIAILTGG 296


RESULT 13
CH60_CLOTM
ID   CH60_CLOTM     STANDARD;      PRT;   540 AA.
AC   P48212;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein) (HSP-60).
GN   GROL OR MOPA OR GROEL.
OS   Clostridium thermocellum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1515;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCIB 10682;
RX   MEDLINE=97199381; PubMed=9047357;
RA   Ciruela A., Cross S., Freedman R.B., Hazlewood G.P.;
RT   "Sequence and transcriptional analysis of groES and groEL genes from
RT   the thermophilic bacterium Clostridium thermocellum.";
RL   Gene 186:143-147(1997).
RN   [2]
RP   SEQUENCE OF 1-20.
RC   STRAIN=NCIB 10682;
RX   MEDLINE=96257758; PubMed=8687408;
RA   Cross S.J., Ciruela A., Poomputsa K., Romaniec M.P.M., Freedman R.B.;
RT   "Thermostable chaperonin from Clostridium thermocellum.";
RL   Biochem. J. 316:615-622(1996).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; Z68137; CAA92242.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding.
FT   INIT_MET      0      0
FT   CONFLICT     14     15       LE -> ML (IN REF. 2).
FT   CONFLICT     20     20       Q -> K (IN REF. 2).
SQ   SEQUENCE   540 AA;  57343 MW;  A638C71A2675C596 CRC64;

  Query Match             4.6%;  Score 25;  DB 1;  Length 540;
  Best Local Similarity   100.0%;  Pred. No. 3e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    272 VAVKAPGFGDRRKAMLEDIAILTGG 296
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          ||||||||||||||||||||||||
Db    271 VAVKAPGFGDRRKAMLEDIAILTGG 295


RESULT 14
CH60_BACHD
ID   CH60_BACHD     STANDARD;      PRT;   544 AA.
AC   O50305; Q9KFC3;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL OR BH0562.
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=97141316; PubMed=8987660;
RA   Xu Y., Kobayashi T., Kudo T.;
RT   "Molecular cloning and nucleotide sequence of the groEL gene from the
RT   alkaliphilic Bacillus sp. strain C-125 and reactivation of thermally
RT   inactivated alpha-glucosidase by recombinant GroEL.";
RL   Biosci. Biotechnol. Biochem. 60:1633-1636(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- INDUCTION: BY HEAT SHOCK.
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D55630; BAA09494.1; -.
DR   EMBL; AP001508; BAB04281.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding; Heat shock; Complete proteome.
FT   CONFLICT    407    407       E -> VK (IN REF. 1).
FT   CONFLICT    421    421       MISSING (IN REF. 1).
FT   CONFLICT    500    500       A -> VP (IN REF. 1).
FT   CONFLICT    512    512       MISSING (IN REF. 1).
SQ   SEQUENCE   544 AA;  57403 MW;  C769ED81C903C971 CRC64;

  Query Match             4.6%;  Score 25;  DB 1;  Length 544;
  Best Local Similarity   100.0%;  Pred. No. 3e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    272 VAVKAPGFGDRRKAMLEDIAILTGG 296
          |||||||||||||||||||||||||
Db    272 VAVKAPGFGDRRKAMLEDIAILTGG 296


RESULT 15
CH60_BURCE
ID   CH60_BURCE     STANDARD;      PRT;   546 AA.
AC   Q9ZFE0;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   60 kDa chaperonin (Protein Cpn60) (groEL protein).
GN   GROL OR MOPA OR GROEL.
OS   Burkholderia cepacia (Pseudomonas cepacia).
OC   Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC   Burkholderia.
OX   NCBI_TaxID=292;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NCTC 10744;
RA   Zysk G., Splettstoesser W.D., Neubauer H.;
RT   "Nucleotide sequence comparison of the groE operon of Burkholderia
RT   spp.";
RL   Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC       PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC       CONDITIONS (BY SIMILARITY).
CC   -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC       7 SUBUNITS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF104907; AAC79087.1; -.
DR   HSSP; P06139; 1GRL.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW   Chaperone; ATP-binding.
SQ   SEQUENCE   546 AA;  56980 MW;  174B9934345E7315 CRC64;

  Query Match             4.6%;  Score 25;  DB 1;  Length 546;
  Best Local Similarity   100.0%;  Pred. No. 3e-14;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    272 VAVKAPGFGDRRKAMLEDIAILTGG 296
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Db    274 VAVKAPGFGDRRKAMLEDIAILTGG 298


Search completed: April  8, 2003, 14:35:39
Job time : 28 secs
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